



THE KENNEL CLUB

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September 2015

Population analysis of the *Chinese Crested* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Chinese Crested*** population has been carried out with the aim of estimating the rate of loss of genetic diversity within the breed and providing information to guide a future sustainable breeding strategy. The population statistics summarised provide a picture of trends in census size, the number of animals used for breeding, the rate of inbreeding and the estimated effective population size. The rate of inbreeding and estimated effective population size indicate the rate at which genetic diversity is being lost within the breed. The analysis also calculates the average relationship (kinship) among all individuals of the breed born per year and is used to determine the level of inbreeding that might be expected if matings were made among randomly selected dogs from the population (the expected rate of inbreeding).

Summary of results

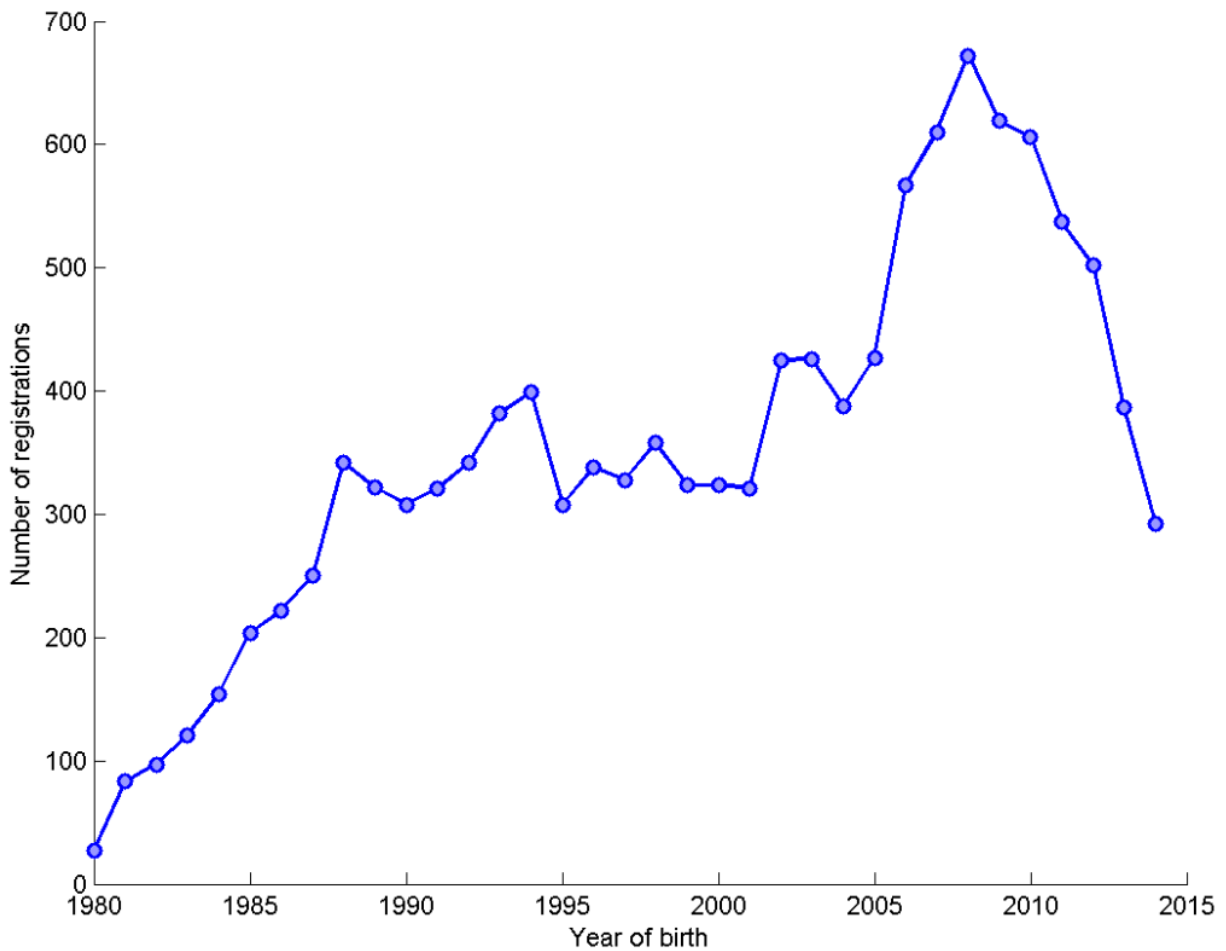
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Chinese Crested*** population, and statistics were calculated for the period 1980-2014.



Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Chinese Crested

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 12.53 per year (with a 95% confidence interval of 9.47 to 15.59).



Table 1: census statistics by year, including sire use statistics.

Table 1: by year (1980-2014), the number of registered puppies born, by the number of unique dams and sires; maximum, median, mode, mean and standard deviation of number of puppies per sire; and the percentage of all puppies born to the most prolific 50%, 25%, 10% and 5% of sires.

year	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	27	17	12	8	1	1	2.25	2.18	77.78	59.26	29.63	29.63
1981	83	42	29	10	2	1	2.86	2.23	77.11	51.81	28.92	12.05
1982	97	51	36	7	2	2	2.69	1.82	74.23	49.48	26.8	14.43
1983	121	59	38	13	3	1	3.18	2.68	78.51	56.2	30.58	17.36
1984	154	72	48	11	2	1	3.21	2.61	79.22	54.55	28.57	12.99
1985	204	88	54	13	3	2	3.78	3.05	76.96	54.41	27.94	18.14
1986	222	92	60	13	3	1	3.7	2.91	79.28	52.25	28.38	15.77
1987	250	100	65	14	3	1	3.85	2.72	77.6	48.4	26.4	13.2
1988	342	122	73	18	4	4	4.68	3.98	78.65	54.09	30.12	19.3
1989	322	109	67	18	4	4	4.81	3.82	75.78	53.11	30.75	15.22
1990	308	112	73	16	3	3	4.22	2.97	75.32	48.38	24.35	16.23
1991	321	109	75	14	3	3	4.28	2.96	75.39	49.53	27.41	15.58
1992	342	110	73	16	3	2	4.68	3.41	78.07	51.46	23.98	14.91
1993	382	125	84	25	3	1	4.55	4.26	79.32	57.07	31.68	19.11
1994	399	130	90	16	4	2	4.43	3.29	77.19	51.63	26.82	17.04
1995	308	117	80	15	3	1	3.85	3.11	77.92	53.9	28.25	16.88
1996	338	110	77	21	4	2	4.39	3.42	77.22	49.11	27.22	17.75
1997	328	113	78	28	3	1	4.21	4.44	79.27	56.71	33.54	23.48
1998	358	112	81	18	3	3	4.42	3.56	76.26	51.96	29.33	17.6
1999	324	126	80	14	3	1	4.05	3.31	78.7	54.63	29.01	16.36
2000	324	112	74	14	3	3	4.38	3.37	77.78	53.4	26.54	16.67
2001	321	111	71	19	4	2	4.52	3.46	78.5	51.09	27.1	17.13
2002	425	135	93	22	4	1	4.57	3.77	78.12	52.24	28.71	19.06
2003	426	137	94	23	4	2	4.53	3.51	76.06	50.94	26.76	17.37
2004	388	124	87	18	3	1	4.46	3.65	80.41	54.64	28.61	15.46
2005	427	146	92	21	4	1	4.64	3.98	82.44	55.04	28.34	17.56
2006	567	179	126	22	3	1	4.5	4.16	82.54	58.02	31.75	17.81
2007	610	175	120	34	4	1	5.08	5.01	82.46	57.38	32.13	20.49
2008	672	194	143	21	4	3	4.7	3.61	77.98	52.38	27.23	15.63
2009	619	184	131	39	4	1	4.73	4.59	79.81	54.6	30.69	20.36
2010	606	184	133	23	3	2	4.56	4.29	79.37	55.45	32.67	21.78
2011	537	162	124	25	4	1	4.33	3.58	78.4	50.47	27.37	17.32
2012	502	160	124	20	3	1	4.05	3.5	79.28	54.18	29.88	17.93
2013	387	123	99	18	3	1	3.91	3.38	79.84	54.78	30.49	18.09
2014	292	86	64	21	4	1	4.56	3.73	76.71	52.4	27.4	16.78

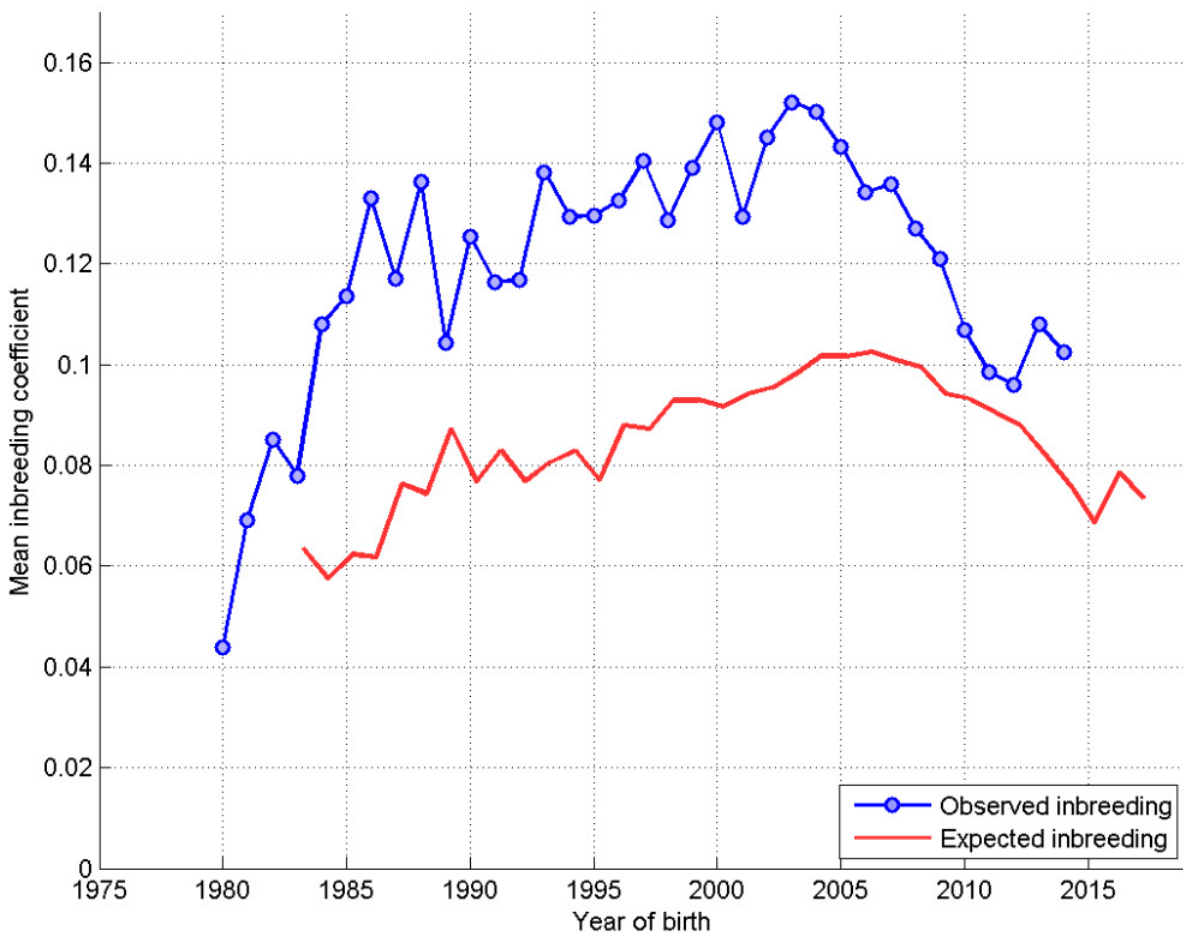


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.24

Figure 2: a plot of the annual mean observed inbreeding coefficient (showing loss of genetic diversity), and mean expected inbreeding coefficient (from 'random mating') over the period 1980-2014. 'Expected inbreeding' is staggered by the generation interval and, where >2000 animals are born in a single year, the 95% confidence interval is indicated.

Figure 2: Annual mean observed and expected inbreeding coefficients





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Estimated effective population size: the rate of inbreeding (slope or steepness of the observed inbreeding in Figure 2) is used to estimate the effective population size of the breed. The effective population size is the number of breeding animals in an idealised, hypothetical population that would be expected to show the same rate of loss of genetic diversity (rate of inbreeding) as the breed in question. It may be thought of as the size of the 'gene pool' of the breed.

Below an effective population size of 100 (inbreeding rate of 0.50% per generation) the rate of loss of genetic diversity in a breed/population increases dramatically (Food & Agriculture Organisation of the United Nations, "Monitoring animal genetic resources and criteria for prioritization of breeds", 1992). An effective population size of below 50 (inbreeding rate of 1.0% per generation) indicates the future of the breed may be considered to be at risk (Food & Agriculture Organisation of the United Nations, "Breeding strategies for sustainable management of animal genetic resources", 2010).

Where the rate of inbreeding is negative (implying *increasing* genetic diversity in the breed), effective population size is denoted 'n/a'.

Estimated effective population size = 159.3

NB - this estimate is made using the rate of inbreeding over the whole period 1980-2014



Table 2: a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the trend in observed inbreeding in Figure 2.

Table 2: by 5-year blocks, the mean number of registrations; for sires the total number used, maximum, mean, median, mode, standard deviation and skewness (indicative of the size of the 'tail' on the distribution) of number of progeny per sire; for dams the total number used, maximum, mean, median, mode, standard deviation and skewness of number of progeny per dam; rate of inbreeding per generation (as a decimal, multiply by 100 to obtain as a percentage); mean generation interval; and estimated effective population size.

years	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014
Mean #registrations	96.4	268	350.4	331.2	376.8	579	464.8
Total #sires	96	194	247	251	276	408	377
Max #progeny	27	41	46	50	38	63	59
Mean #progeny	5.0104	6.8866	7.0891	6.5936	6.8225	7.0931	6.1618
Median #progeny	3	4	5	4	5	4	4
Mode #progeny	1	3	2	1	1	1	1
SD #progeny	4.9236	7.5094	7.0134	7.1096	6.4058	8.3808	6.9998
Skew #progeny	1.9991	2.258	2.0312	2.5865	1.8232	2.5556	3.2709
Total #dams	161	340	408	398	437	631	544
Max #progeny	11	18	16	19	23	24	23
Mean #progeny	2.9876	3.9382	4.2917	4.1583	4.3089	4.5864	4.2702
Median #progeny	2	3	3	3	4	4	3
Mode #progeny	1	3	2	3	1	1	1
SD #progeny	2.1966	2.822	3.0428	3.2046	3.3474	3.8953	3.6077
Skew #progeny	1.3469	1.4456	1.3704	1.5595	1.7278	1.6902	1.7917
Rate of inbreeding	0.041928	-0.0055	0.010521	0.00584	0.010436	-0.01931	0.00028
Generation interval	2.8485	3.2575	3.0987	3.3057	3.3232	3.2209	3.6442
Effective pop size	11.925	n/a	47.522	85.612	47.913	n/a	1787



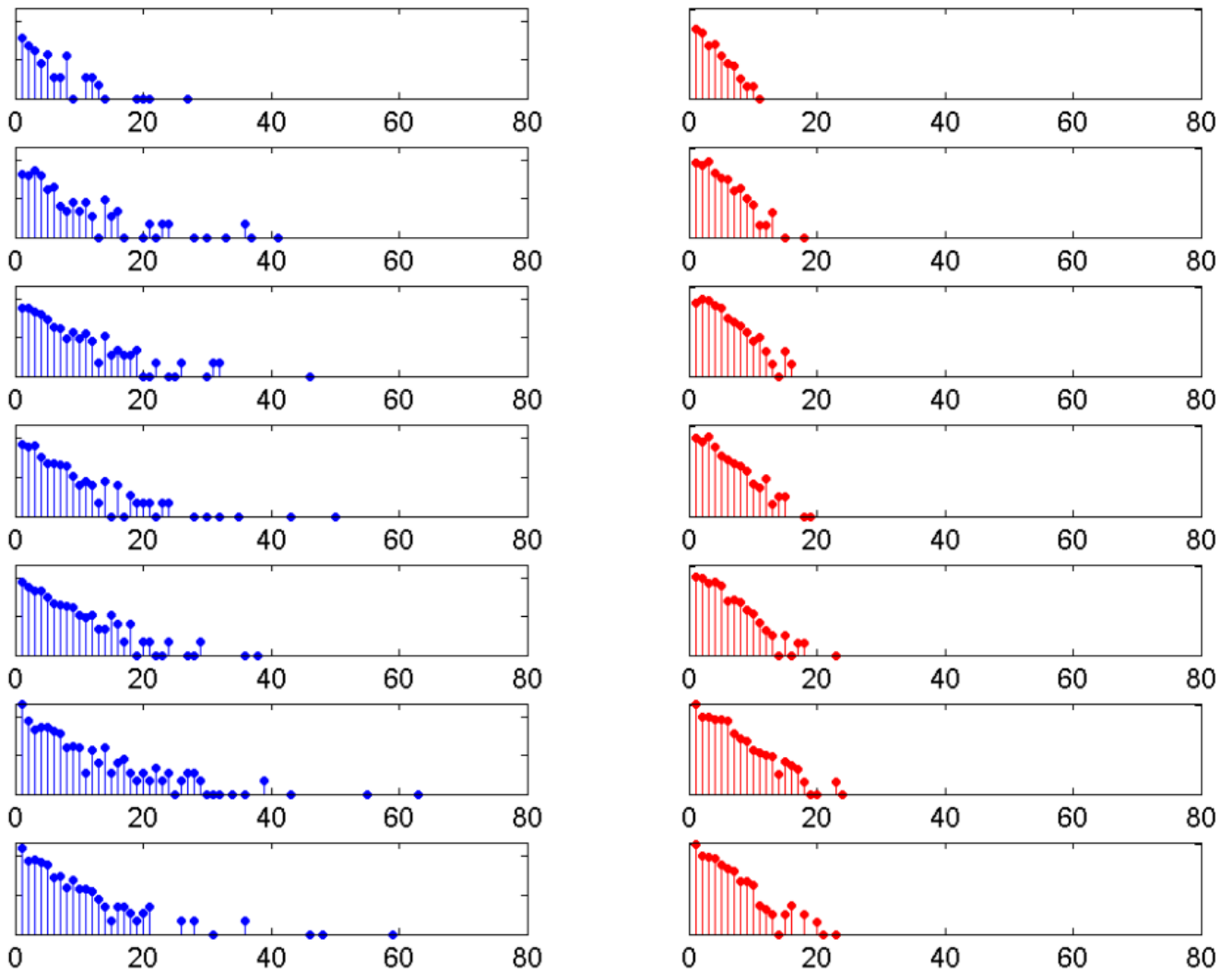
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number of offspring, known to be a major contributor to a high rate of inbreeding).

Figure 3: Distribution of progeny per sire (blue) and per dam (red) over 5-year blocks (1980-4 top, 2010-14 bottom). Vertical axis is a logarithmic scale.





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Comments

The rate of inbreeding was at its highest in this breed in the early 1980s. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, the rate of inbreeding has since slowed and even declined latterly, implying a slowdown in the rate of loss and even some replenishment of genetic diversity (possibly through the use of imported animals).

There appears to be moderate use of popular dogs as sires in this breed (the 'tail' of the blue distribution in figure 3).

It should be noted that, while animals imported from overseas may appear completely unrelated, this is not always the case. Often the pedigree available to the Kennel Club is limited in the number of generations, hampering the ability to detect true, albeit distant, relationships.